

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Hillman, Jennifer L.
Corley, Neil C.
Baughn, Mariah R.

(ii) TITLE OF INVENTION: DELTA 1-PYRROLINE-5-CARBOXYLATE REDUCTASE
HOMOLOG

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: Windows
(D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: TO BE ASSIGNED
(B) FILING DATE: HEREWITH
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Cerrone, Michael C
(B) REGISTRATION NUMBER: 39,132
(C) REFERENCE/DOCKET NUMBER: PF-0532 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-855-0572
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: PROSNON01

(B) CLONE: 2278458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ser Val Gly Phe Ile Gly Ala Gly Gln Leu Ala Tyr Arg Phe Thr
 1 5 10 15
 Ala Ala Gly Ile Leu Ser Ala His Lys Ile Ile Ala Ser Ser Pro Glu
 20 25 30
 Met Asn Leu Pro Thr Val Ser Ala Leu Arg Lys Met Gly Val Asn Leu
 35 40 45
 Thr Arg Ser Asn Lys Glu Thr Val Lys His Ser Asp Val Leu Phe Leu
 50 55 60
 Ala Val Lys Pro His Ile Ile Pro Phe Ile Leu Asp Glu Ile Gly Ala
 65 70 75 80
 Asp Val Gln Ala Arg His Ile Val Val Ser Cys Ala Ala Gly Val Thr
 85 90 95
 Ile Ser Ser Val Glu Lys Lys Leu Met Ala Phe Gln Pro Ala Pro Lys
 100 105 110
 Val Ile Arg Cys Met Thr Asn Thr Pro Val Val Val Gln Glu Gly Ala
 115 120 125
 Thr Val Tyr Ala Thr Gly Thr His Ala Leu Val Glu Asp Gly Gln Leu
 130 135 140
 Leu Glu Gln Leu Met Ser Ser Val Gly Phe Cys Thr Glu Val Glu Glu
 145 150 155 160
 Asp Leu Ile Asp Ala Val Thr Gly Leu Ser Gly Ser Gly Pro Ala Tyr
 165 170 175
 Ala Phe Met Ala Leu Asp Ala Asp Gly Gly Val Lys Met Gly Leu Pro
 180 185 190
 Arg Arg Leu Ala Ile Gln Leu Gly Ala Gln Ala Leu Leu Gly Ala Ala
 195 200 205
 Lys Met Leu Leu Asp Ser Glu Gln His Pro Cys Gln Leu Lys Asp Asn
 210 215 220
 Val Cys Ser Pro Gly Gly Ala Thr Ile His Ala Leu His Phe Leu Glu
 225 230 235 240
 Ser Gly Gly Phe Arg Ser Leu Leu Ile Asn Ala Val Glu Ala Ser Cys
 245 250 255
 Ile Arg Thr Arg Glu Leu Gln Ser Met Ala Asp Gln Glu Lys Ile Ser
 260 265 270
 Pro Ala Ala Leu Lys Lys Thr Leu Leu Asp Arg Val Lys Leu Glu Ser
 275 280 285
 Pro Thr Val Ser Thr Leu Thr Pro Ser Ser Pro Gly Lys Leu Leu Thr
 290 295 300
 Arg Ser Leu Ala Leu Gly Gly Lys Lys Asp
 305 310

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1742 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNON01
- (B) CLONE: 2278458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | |
|---|-----|
| GCGCCATCAG CCGCCCGGGA GATATCCGCC GGGGGAGAAT AGGGTTGCAC CATCCCAGAA | 60 |
| GCTGCTGTTA GCTCGCCGGT CCTCGGCACG CGGCCCGTTC GCCCCTGCGC TGTCCGCCCT | 120 |

| | | | | | | |
|-------------|------------|-------------|-------------|------------|-------------|------|
| TCCCCCTAGCG | TTACTTCCGG | TCCCTCGCTG | AGGGGGTTCG | TGCGGCCTCC | AGGAGGCGTG | 180 |
| AACCGCGGAC | CATGAGCGTG | GGCTTCATCG | GGGCCGGCCA | GCTGGCCTAT | GCTCTGGCGC | 240 |
| GGGGCTTCAC | GGCCGCAGGC | ATCCTGTCGG | CTCACAAAGAT | AATAGCCAGC | TCCCCAGAAA | 300 |
| TGAACCTGCC | CACGGTGTCC | GCGCTCAGGA | AGATGGGTGT | GAACCTGACA | CGCAGCAACA | 360 |
| AGGAGACGGT | GAAGCACAGC | GACGTCCGT | TTCTGGCTGT | GAAGCCACAT | ATCATCCCCT | 420 |
| TCATCCTGGA | TGAGATTGGG | GCCGACGTGC | AAGCCAGACA | CATCGTGGTC | TCCTGTGCGG | 480 |
| CTGGTGTAC | CATCAGCTCT | GTGGAGAAGA | AGCTGATGGC | ATTCCAGCCA | GCCCCCAAAG | 540 |
| TGATTCGCTG | CATGACCAAC | ACACCTGTGG | TAGTGCAGGA | AGGCGCTACA | GTGTACGCCA | 600 |
| CGGGCACCCA | TGCCCTGGTG | GAGGATGGGC | AGCTCCTGGA | GCAGCTCATG | AGCAGCGTGG | 660 |
| GCTTCTGCAC | TGAGGTGGAA | GAGGACCTCA | TCGATGCCGT | CACGGGGCTC | AGTGGCAGCG | 720 |
| GGCCTGCCTA | TGCATTCATG | GCTCTGGACG | CATTGGCTGA | TGGTGGGTG | AAGATGGGTT | 780 |
| TGCCACGGCG | CCTGGCAATC | CAACTCGGGG | CCCAGGCTTT | GCTGGGAGCT | GCCAAGATGC | 840 |
| TGCTGGACTC | GGAGCAGCAT | CCATGCCAGC | TTAAGGACAA | TGTCTGCTCC | CCTGGGGGAG | 900 |
| CCACCATCCA | CGCCCTGCAC | TTTCTAGAGA | GTGGGGGCTT | CCGCTCTCTG | CTCATCAATG | 960 |
| CAGTTGAGGC | CTCCTGTATC | CGAACACGAG | AGCTACAGTC | CATGGCCGAC | CAAGAAAAGA | 1020 |
| TCTCCCCAGC | TGCCCTTAAG | AAGACCTCT | TAGACAGAGT | GAAGCTGGAA | TCCCCCACAG | 1080 |
| TCTCCACACT | GACCCTCTCC | AGCCCAGGA | AGCTCCTCAC | AAGAACCTG | GCCCTGGGAG | 1140 |
| GCAAGAAGGA | CTAAGGCAGC | ATCTGTCCCC | TCTGTGATTG | AGAGCCCTTA | GTGAGAGCC | 1200 |
| CCTGCCGCC | CTGCCACCCC | CCTGCCCGC | TCCCACCATT | GCCCCTCCTC | AGCTGTGCAA | 1260 |
| GGAGAAAGCA | TGCTTAGGAA | GTTTTCAGGT | CCTTGTGATA | AAACCTCCTT | AAATCTGTT | 1320 |
| AGACCAAGCA | ATGCGAGCTT | CCTCTCCTGT | CCCATGTTGG | AAGTTGCTCT | GAAGGGGTGG | 1380 |
| TAGATGCTGG | AAGCCAGACA | CAACCCCTGCG | TACGCTGCTC | AGTTGGTGG | GACTGGGGCT | 1440 |
| GGGACTGGAG | TCAGCCCAGC | TGGGAGGAGG | GGCTGGGGAG | GATCTGCAGC | TGAAGCCCCGA | 1500 |
| GGCAGGGTTG | GTGTGATGCC | AAGGCAAAGT | GGTGAGGAGA | AAACAGGAAA | CGGGCTTTCT | 1560 |
| CTGAATTGGT | AAATGGGAAA | GAAGTGAGCA | ACTTAAGATT | GTCACAATTA | ATCACAAAGTG | 1620 |
| TACAGGATTA | GACTGGGTTT | ATATTAACT | CTTGCTTCAT | AGGTGTACCA | TTTAAAGAGT | 1680 |
| GTTATTAAAT | GCTAAGTTTA | ACTGCTTAA | TAAAGTTAT | TTTAAATAT | CAAAAAAAA | 1740 |
| AA | | | | | | 1742 |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GENBANK
- (B) CLONE: 189498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Val | Gly | Phe | Ile | Gly | Ala | Gly | Gln | Leu | Ala | Phe | Ala | Lys | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Phe | Thr | Ala | Ala | Gly | Val | Leu | Ala | Ala | His | Lys | Ile | Met | Ala | Ser | Ser |
| | | | | | | | | | 20 | | | 25 | | 30 | |
| Pro | Asp | Met | Asp | Leu | Ala | Thr | Val | Ser | Ala | Leu | Arg | Lys | Met | Gly | Val |
| | | | | | | | | | 35 | | | 40 | | 45 | |
| Lys | Leu | Thr | Pro | His | Asn | Lys | Glu | Thr | Val | Gln | His | Ser | Asp | Val | Leu |
| | | | | | | | | | 50 | | | 55 | | 60 | |
| Phe | Leu | Ala | Val | Lys | Pro | His | Ile | Ile | Pro | Phe | Ile | Leu | Asp | Glu | Ile |
| | | | | | | | | | 65 | | | 70 | | 75 | |
| Gly | Ala | Asp | Ile | Glu | Asp | Arg | His | Ile | Val | Val | Ser | Cys | Ala | Ala | Gly |
| | | | | | | | | | 85 | | | 90 | | 95 | |
| Val | Thr | Ile | Ser | Ser | Ile | Glu | Lys | Lys | Leu | Ser | Ala | Phe | Arg | Pro | Ala |
| | | | | | | | | | 100 | | | 105 | | 110 | |
| Pro | Arg | Val | Ile | Arg | Cys | Met | Thr | Asn | Thr | Pro | Val | Val | Val | Arg | Glu |
| | | | | | | | | | 115 | | | 120 | | 125 | |
| Gly | Ala | Thr | Val | Tyr | Ala | Thr | Gly | Thr | His | Ala | Gln | Val | Glu | Asp | Gly |
| | | | | | | | | | 130 | | | 135 | | 140 | |

Arg Leu Met Glu Gln Leu Leu Ser Thr Val Gly Phe Cys Thr Glu Val
145 150 155 160
Glu Glu Asp Leu Ile Asp Ala Val Thr Gly Leu Ser Gly Ser Gly Pro
165 170 175
Ala Tyr Ala Phe Thr Ala Leu Asp Ala Asp Gly Gly Val Lys Met Gly
180 185 190
Leu Pro Arg Arg Leu Ala Val Arg Leu Gly Ala Gln Ala Leu Leu Gly
195 200 205
Ala Ala Lys Met Leu Leu His Ser Glu Gln His Pro Gly Gln Leu Lys
210 215 220
Asp Asn Val Ser Ser Pro Gly Gly Ala Thr Ile His Ala Leu His Val
225 230 235 240
Leu Glu Ser Gly Gly Phe Arg Ser Leu Leu Ile Asn Ala Val Glu Ala
245 250 255
Ser Cys Ile Arg Thr Arg Glu Leu Gln Ser Met Ala Asp Gln Glu Gln
260 265 270
Val Ser Pro Ala Ala Ile Lys Lys Thr Ile Leu Asp Lys Val Lys Leu
275 280 285
Asp Ser Pro Ala Gly Thr Ala Leu Ser Pro Ser Gly His Thr Lys Leu
290 295 300
Leu Pro Arg Ser Leu Ala Pro Ala Gly Lys Asp
305 310 315